

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10 | S24,278

Source:

PGT

Date Processed by STIC:

2-23-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/5241278

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220> <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220> <223> section is required when <213> response is Unknown or Artificial Sequence.
- 11 Use of <220>
 Sequence(s) missing the <220> feature and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (Sec "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING

DATE: 02/23/2005

PATENT APPLICATION: US/10/524,278

TIME: 09:14:58

Input Set : A:\3190-074 Sequence Listing.txt

Output Set: N:\CRF4\02232005\J524278.raw

3 <110> APPLICANT: SATO, Hiroshi
 4 FUJIYAMA, Yoshihide
 5 YAMAMOTO, Kazuo
 7 <120> TITLE OF INVENTION: Method for Predicting Drug Metabolizing Activity by Analysis
 of
 8 Glucuronosyltransferase Gene Mutation
 10 <130> FILE REFERENCE: 3190-074
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/524,278
 13 <141> CURRENT FILING DATE: 2005-02-09
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/01475
 16 <151> PRIOR FILING DATE: 2003-02-13
 18 <150> PRIOR APPLICATION NUMBER: JP P2002-235029
 19 <151> PRIOR FILING DATE: 2002-08-12
 21 <160> NUMBER OF SEQ ID NOS: 11
 23 <170> SOFTWARE: PatentIn version 3.1

Does Not Comply
 Corrected Diskette Needed

(pg. 1-2)

ERRORED SEQUENCES

156 <210> SEQ ID NO: 10
 157 <211> LENGTH: 24
 158 <212> TYPE: DNA
 159 <213> ORGANISM: Artificial
 161 <220> FEATURE:
 162 <223> OTHER INFORMATION: Designed DNA based on UGT1 gene
 164 <400> SEQUENCE: 10
 165 ccgcagccca cgacctcacc.tggt
 E--> 171
 174 <210> SEQ ID NO: 11
 175 <211> LENGTH: 24
 176 <212> TYPE: DNA
 177 <213> ORGANISM: Artificial
 179 <220> FEATURE:
 180 <223> OTHER INFORMATION: Designed DNA based on UGT gene
 182 <400> SEQUENCE: 11
 183 agaggaaacc aatcacgtcc'aagg
 E--> 228

PLS
 -3- delete

24

PLS
 -4- delete

24

→ FYI:
Page numbers are not
allowed in Raw Sequence listings

<210> 7

<211> 21

<212> DNA

<213> Artificial

Pls explain source of genetic material.

<220>

<223> 21

What is this?

<400> 7

agatgcagag ctcaataggt c

21

↑ See item # 11 on
error summary sheet.

↑

The type of errors shown exist throughout
the sequence listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/524,278

DATE: 02/23/2005
TIME: 09:14:59

Input Set : A:\3190-074 Sequence Listing.txt
Output Set: N:\CRF4\02232005\J524278.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/524,278

DATE: 02/23/2005

TIME: 09:14:59

Input Set : A:\3190-074 Sequence Listing.txt

Output Set: N:\CRF4\02232005\J524278.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:59 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:171 M:254 E: No. of Bases conflict, this line has no nucleotides. /
L:228 M:254 E: No. of Bases conflict, this line has no nucleotides. /